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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/764,163A

DATE: 05/14/2003

TIME: 07:09:34

Input Set : A:\-7-1.app

Output Set: N:\CRF4\05142003\I764163A.raw

3 <110> APPLICANT: Balint, Robert F.
 4 Her, Jeng-Horng
 5 KaloBios, Inc.
 7 <120> TITLE OF INVENTION: Circularly Permutated, Interaction-Activated Proteins
 9 <130> FILE REFERENCE: 021167-000710US
 11 <140> CURRENT APPLICATION NUMBER: US 09/764,163A
 12 <141> CURRENT FILING DATE: 2001-01-16
 14 <150> PRIOR APPLICATION NUMBER: US 60/175,968
 15 <151> PRIOR FILING DATE: 2000-01-13
 17 <150> PRIOR APPLICATION NUMBER: US 09/526,106
 18 <151> PRIOR FILING DATE: 2000-03-15
 20 <160> NUMBER OF SEQ ID NOS: 26
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 789
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Escherichia coli
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(789)
 32 <223> OTHER INFORMATION: TEM-1 beta-lactamase
 34 <400> SEQUENCE: 1
 35 cac cca gaa acg ctg gtg aaa gta aaa gat gct gaa gat cag ttg ggt 48
 36 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 37 1 5 10 15
 39 gca cga gtg ggt tac atc gaa ctg gat ctc aac agc ggt aag atc ctt 96
 40 Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 41 20 25 30
 43 gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa 144
 44 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
 45 35 40 45
 47 gtt ctg cta tgt ggc gcg gta tta tcc cgt att gac gcc ggg caa gag 192
 48 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
 49 50 55 60
 51 caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt gag tac 240
 52 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 53 65 70 75 80
 55 tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga gaa 288
 56 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 57 85 90 95
 59 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta 336
 60 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 61 100 105 110

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63 ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt ttg cac 384
64 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
65      115      120      125
67 aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg 432
68 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
69      130      135      140
71 aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct gta gca 480
72 Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
73 145      150      155      160
75 atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt act cta 528
76 Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
77      165      170      175
79 gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa gtt gca 576
80 Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
81      180      185      190
83 gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att gct gat 624
84 Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
85      195      200      205
87 aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca gca ctg 672
88 Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
89      210      215      220
91 ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg acg ggg 720
92 Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
93 225      230      235      240
95 agt cag gca act atg gat gaa cga aat aga cag atc gct gag ata ggt 768
96 Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
97      245      250      255
99 gcc tca ctg att aag cat tgg 789
100 Ala Ser Leu Ile Lys His Trp
101      260
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 263
106 <212> TYPE: PRT
107 <213> ORGANISM: Escherichia coli
109 <220> FEATURE:
110 <223> OTHER INFORMATION: TEM-1 beta-lactamase
112 <400> SEQUENCE: 2
113 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
114 1      5      10      15
116 Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
117      20      25      30
119 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
120      35      40      45
122 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
123      50      55      60
125 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
126 65      70      75      80
128 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
129      85      90      95

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131 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
132          100          105          110
134 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
135          115          120          125
137 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
138          130          135          140
140 Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
141 145          150          155          160
143 Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
144          165          170          175
146 Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
147          180          185          190
149 Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
150          195          200          205
152 Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
153          210          215          220
155 Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
156 225          230          235          240
158 Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
159          245          250          255
161 Ala Ser Leu Ile Lys His Trp
162          260
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 5
167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
173 <400> SEQUENCE: 3
174 Gly Gly Gly Gly Ser
175 1          5
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 15
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence:flexible linker
186 <400> SEQUENCE: 4
187 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
188 1          5          10          15
191 <210> SEQ ID NO: 5
192 <211> LENGTH: 6
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence:hexa-histidine
198 tag
200 <400> SEQUENCE: 5
201 His His His His His His

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202      1              5
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 5
207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Description of Artificial Sequence:flexible linker
212      of variable length
214 <220> FEATURE:
215 <221> NAME/KEY: REPEAT
216 <222> LOCATION: (1)..(5)
217 <223> OTHER INFORMATION: (G-4S)-x, amino acids 1-5 may be repeated an
218      undefined number of times
220 <400> SEQUENCE: 6
221 Gly Gly Gly Gly Ser
222      1              5
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 267
227 <212> TYPE: PRT
228 <213> ORGANISM: Escherichia coli
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Neomycin phosphotransferase II (NPTII)
233 <400> SEQUENCE: 7
234 Met Gly Ser Ala Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala
235      1              5              10              15
237 Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile
238      20              25              30
240 Gly Cys Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro
241      35              40              45
243 Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln
244      50              55              60
246 Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys
247      65              70              75              80
249 Ala Ala Val Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu
250      85              90              95
252 Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro
253      100             105             110
255 Ala Glu Lys Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr
256      115             120             125
258 Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile
259      130             135             140
261 Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp
262      145             150             155             160
264 Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg
265      165             170             175
267 Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly
268      180             185             190
270 Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly
271      195             200             205

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273 Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile
274      210      215      220
276 Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala
277 225      230      235      240
279 Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg
280      245      250      255
282 Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe
283      260      265
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 18
288 <212> TYPE: PRT
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
293      Trxpep
295 <400> SEQUENCE: 8
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297 1      5      10      15
299 Pro Cys
302 <210> SEQ ID NO: 9
303 <211> LENGTH: 18
304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
309      Trxpep
311 <400> SEQUENCE: 9
312 Cys Gly Pro Glu Gly Gln Gly Gly Val Ala Val Gly Gly Val Gly Gly
313 1      5      10      15
315 Pro Cys
318 <210> SEQ ID NO: 10
319 <211> LENGTH: 16
320 <212> TYPE: PRT
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
325      Trxpep
327 <400> SEQUENCE: 10
328 Cys Gly Pro Ala Lys Arg Ala Asp Val Glu Phe Ser Leu Glu Pro Gly
329 1      5      10      15
332 <210> SEQ ID NO: 11
333 <211> LENGTH: 21
334 <212> TYPE: PRT
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
339      Trxpep
341 <400> SEQUENCE: 11
342 Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu

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VERIFICATION SUMMARY

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